

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 17, 2001, 21:52:24 ; Search time 71.96 seconds  
(without alignments)  
259,843 Million cell updates/sec

Title: US-09-456-306-2

Peptide score: 2965  
Sequence: 1 MAHSVABQLIDTLEAGVKR.....GGVGAMIDLANSRINRITPT 579

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1317.5	44.1	572	1	POXB_ECOLI
2	902.5	30.2	396	1	Y142_PSEAY
3	586.5	19.6	591	1	ILVB_METYA
4	560	18.8	603	1	POXB_LACPL
5	554.5	18.6	573	1	ILVB_BACSU
6	533.5	17.9	575	1	ILVB_GUTH
7	533.5	17.9	590	1	ILVB_PORPU
8	523.5	17.6	618	1	ILVB_MYCTU
9	523.5	17.5	562	1	ILVB_ECOTL
10	517.5	17.3	579	1	ILVB_ECOTL
11	507	17.0	548	1	ILVB_ECOTL
12	503	16.9	625	1	ILVB_MYCLE
13	493	16.5	670	1	ILVB_ARATH
14	482	16.5	591	1	POXB_STRPN
15	480	16.1	655	1	ILV3_BRANA
16	477	16.0	652	1	ILV3_BRANA
17	464.5	15.6	621	1	ILVB_MYCAV
18	461	15.4	626	1	ILVB_CORGL
19	454	15.2	664	1	ILV2_TOBAC
20	449	15.2	667	1	ILV1_TOBAC
21	449	15.0	575	1	ILVB_LACLA
22	441.5	14.8	637	1	ILV2_BRANA
23	442	14.1	559	1	ILVB_KLETE
24	440	14.1	574	1	ILV1_ECOTL
25	418.5	14.0	669	1	ILVB_SCHPO
26	414	13.9	687	1	ILVB_YEAST
27	393	13.2	559	1	ILVB_KLEPN
28	390.5	13.1	573	1	ILV1_NHEIN
29	385.5	12.9	571	1	ILV1_BUCAP
30	356	11.9	592	1	GCL_ECOTL
31	332	11.1	494	1	Y663_METUA
32	316.5	10.6	540	1	ILVX_BACSU
33	313	10.5	547	1	ILVX_MYCTU

34	287.5	9.6	563	1	B2NB_PSEFL
35	282.5	9.5	564	1	OXE_ECOTL
36	274.5	9.2	580	1	IOID_BACSU
37	271	9.1	528	1	MDIC_PSEPU
38	257	8.6	560	1	YECO_YEAST
39	238	8.0	545	1	DCIP_AZOBR
40	222	7.4	568	1	OXE_OXAFO
41	215	7.2	571	1	DCPI_SCHPO
42	196	6.6	552	1	DCIP_ENTMO
43	186.5	6.2	568	1	DCPY_ZYMMO
44	174	5.8	563	1	DCPY_KIULA
45	174	5.8	570	1	DCPY_NEUCR

ALIGNMENTS

RESULT 1	STANDARD:	PRT: 572 AA.
ID POXB_ECOLI		
AC P07003: Q47513; Q47514; Q47515; Q47516; Q47517; Q47518; Q47519;		
AC Q47520;		
DT 01-APR-1988 (Rel. 07, Created)		
DT 01-APR-1988 (Rel. 07, Last sequence update)		
DT 01-OCT-2000 (Rel. 40, Last annotation update)		
DE PYRUVATE DEHYDROGENASE [CYTOCHROME] (EC 1.2.2.2) (PYRUVATE OXIDASE)		
DE (POX) (PYRUVATE DEHYDROGENASE [UBIQUINONE]).		
GN POXB.		
OS Escherichia coli.		
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;		
OC Escherichia.		
RN [1]		
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.		
RC STRAIN-K12:		
RX MEDLINE-86286555; PubMed-3016647;		
RA Grabau C., Cronan J.E., Jr.;		
RT "Nucleotide sequence and deduced amino acid sequence of Escherichia coli pyruvate oxidase, a lipid-activated flavoprotein.";		
RL Nucleic Acids Res. 14:5449-5460(1986).		
RN [2]		
RP SEQUENCE FROM N.A.		
RC STRAIN-K12 / MG1655;		
RX MEDLINE-97426617; PubMed-9278503;		
RA Blattner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,		
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,		
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,		
RA Mau B., Shao Y.;		
RT "The complete genome sequence of Escherichia coli K-12.";		
RL Science 277:1453-1474(1997).		
RN [3]		
RP SEQUENCE FROM N.A.		
RC STRAIN-K12:		
RX MEDLINE-97061202; PubMed-8905232;		
RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,		
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,		
RA Kimura S., Kikugawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,		
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,		
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,		
RA Yano M., Horiiuchi T.;		
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome		
RT corresponding to the 12.7-28.0 min region on the linkage map.";		
RL DNA Res. 3:137-155(1996).		
RN [4]		
RP SEQUENCE FROM N.A., AND MUTAGENESIS.		
RC STRAIN-K12:		
RX MEDLINE-89308683; PubMed-2663858;		
RA Grabau C., Chang Y.Y., Cronan J.E., Jr.;		
RT "Lipid binding by Escherichia coli pyruvate oxidase is disrupted by		
RT small alterations of the carboxyl-terminal region.";		
RL J. Biol. Chem. 264:12510-12519(1989).		
RN [5]		
RP SEQUENCE OF 550-572 FROM N.A.		
RL MEDLINE-86033917; PubMed-3902830;		

RA Recny M.A., Grabau C., Cronan J.E., Jr., Hager L.P.:  
 RT "Characterization of the alpha-peptide released upon protease  
 RT activation of pyruvate oxidase."  
 RL J. Biol. Chem. 260:14287-14291(1985).  
 RP [6]  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RX MEDLINE=94293772; PubMed=8022274;  
 RA Chang Y.Y., Wang A.Y., Cronan J.E., Jr.:  
 RT Expression of Escherichia coli pyruvate oxidase (PoxB) depends on  
 RT the sigma factor encoded by the rpos(katF) gene."  
 RL Mol. Microbiol. 11:1019-1028(1994).  
 CC -1- CATALYTIC ACTIVITY: PYRUVATE + FERRICYTOCHROME B1 + H(2)O = CO(2)  
 CC + ACETATE + FERROCYTOCHROME B1.  
 CC -1- COFACTOR: THIAMINE PYRROPHOSPHATE, FAD AND MAGNESIUM ION.  
 CC -1- SUBUNIT: HOMOTETRAMER.  
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.  
 CC -1- PTM: ACTIVATED BY LIMITED PROTEOLYTIC DIGESTION. THIS CLEAVAGE  
 CC PRODUCES A PEPTIDE (ALPHA-PEPTIDE) AND MIMICS THE ACTIVATION OF  
 CC ENZYME BY PHOSPHOLIPIDS. THE PROTEOLYTIC CLEAVAGE ALSO RESULTS IN  
 CC THE LOSS OF THE HIGH AFFINITY LIPID-BINDING SITE OF THE ENZYME.  
 CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.  
 CC -----  
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 CC -----  
 DR EMBL: X04105; CAA27725.1; -  
 DR EMBL: AE000188; AAC73958.1; -  
 DR EMBL: D90724; BA835585.1; -  
 DR EMBL: S73268; AAB31180.1; -  
 DR EMBL: M28208; AAB59101.1; -  
 DR EMBL: L47688; AAB59102.1; -  
 DR EMBL: L47689; AAB59103.1; -  
 DR EMBL: L47690; AAB59104.1; -  
 DR EMBL: L47691; AAB59105.1; -  
 DR EMBL: L47692; AAB59106.1; -  
 DR EMBL: L47693; AAB59107.1; -  
 DR EMBL: L47694; AAB59108.1; -  
 DR EMBL: L47695; AAB59109.1; -  
 DR PIR: A23648; DEECPC.  
 DR HSSP: P37063; IPOM.  
 DR SWISS-2DPAGE: P07003; COLI.  
 DR ECODBASE: G058.0; 6TH EDITION.  
 DR ECOGENE: Bg10754; POXB.  
 DR INTERPRO: IPR000399; -  
 DR PFAM: PF00205; TPP\_ENZYMES; 1.  
 DR PROSITE: PS00187; TPP\_ENZYMES; 1.  
 DR OXIDOREDUCTASE: Flavoprotein; FAD; Thiamine pyrophosphate; Magnesium;  
 KW Membrane; Lipid-binding.  
 KM PEPTIDE 550 572  
 FT ACT\_SITE 50 50 ALPHA-PEPTIDE.  
 FT MUTAGEN 533 533 BY SIMILARITY.  
 FT MUTAGEN 553 553 A->T: IN POXB11.  
 FT MUTAGEN 560 560 A->V: IN POXB14.  
 FT MUTAGEN 564 564 D->P: IN POXB15; NORMAL ACTIVITY.  
 FT MUTAGEN 572 572 R->G: IN POXB16; LOSS OF ACTIVITY.  
 FT INTERACT LESS WITH MEMBRANES.  
 FT MUTAGEN 549 572 MISSING: IN POXB6.  
 FT MUTAGEN 564 572 MISSING: IN POXB7.  
 FT MUTAGEN 570 572 MISSING: IN POXB8.  
 FT CONFLICT 364 365 OO -> HE (IN REF. 4).  
 FT CONFLICT 414 416 OAL -> HGV (IN REF. 4).  
 SQ SEQUENCE 572 AA; 62011 MW; 57B38B9E3A92BDEA CRC64;

Query Match 44.1%; Score 1317.5; DB 1; Length 572;  
 Best Local Similarity 46.3%; Pred. No. 3.7e-79;  
 Matches 266; Conservative 106; Mismatches 195; Indels 7; Gaps 6;

OY 1 MAHSAEQLIDTLEAGQVKRIYGLVGDLSNPYDAV-ROSDIEWVHNEEAAFAAGAE 59  
 Db 1 MKQVAAVIAKLTLESAGVKRWGVTGDSLNGLSDLSRMGMETEMSTRHEEVAFAAGAE 60  
 OY 60 SLITGELAVCAASCGPGNTHIQGLYSHRNGAKVLAISHIPSAOIGSTFFQETHETL 119  
 Db 61 AQLGELAVCAASCGPGNTHINGLFPCRHRNHWVLAIAHITPSELSGSGFQETHOEL 120  
 OY 120 FKESGCEWNGGEGGERILNHAIGSTMAGKGSVAVIPDIDKEPAGGTYSNSTISS 179  
 Db 121 FRESHCELVSSPEQLPOVLAIMKRAVLNKGVSYYVLPEDAVLKAPBEA-TMHWYHA 179  
 OY 180 GTPVFPDPTEAALVLEANNKASVTLFCGAVKNARQVLEAKIKSPIGALGKQY 239  
 Db 180 PQPVVTPPEELRLKLAQLRYSSNIALMCGSCAGAHKEVEFGAKIKAPVHALRKEH 239  
 OY 240 IOHENPEFVNGSGLLGYACADSAENDLILLTDPFYSPLFKD-NVNOVDINGHIG 298  
 Db 240 VEYDNPVGVGMTGLIGSSGPHTMNADTLVLTQPPRYAFYPTDAKITQIDINPSTIG 299  
 OY 299 RRTVKKYPTGDAVATINILPHYEKTRSFLLDRLMLKAHERKLSVETYNVERHVP 358  
 Db 300 AHSKYDALVGDINKTLRALLPIVEKADRKFLDKALEDY-ROARKGLDLAKSEK--A 356  
 OY 359 IHPEVVASILNELADKDAVFTVDMCNVWHARTIENEGTRDVGSRFGSTANALPHA 418  
 Db 357 IHPYLAQOISHFAADDAIFCDVGTPTVMAARYLK-MNGKRRLIGSFNHSNMAMFOA 415  
 OY 419 IGAGSVDRNRVIMCGGSGMLGELLTYKHLQPLKAVFNNSSLGWKLMLVEGQ 478  
 Db 416 LGAQTEPEROVAMCGSGGSMAGDPLSVQMKLPKIVYFNNSVLGFPAAMEKACQY 475  
 OY 479 PEFGTDEHEVFAELTAAAGIKSVATIDPKVRQDLAEALAPGVLIDVDPNALSTP 538  
 Db 476 LTDGELHDTNFAELAECGITGIRVEKASEVDEALQAFSIDPVLVDVVAKEELAI 535  
 OY 539 PLITWEQWGFSSKATRTVFGGCVAMLDLARSN 572  
 Db 536 POKLEQAKGFSLYMLRAIISGRGEVIELAKTN 569  
 RESULT 2  
 Y142\_PSEAY STANDARD: PRT; 396 AA.  
 AC P10343;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 01-NOV-1990 (Rel. 16, Last annotation update)  
 DE HYPOTHETICAL 42.6 KDA PROTEIN IN ISOMYLASE 3' REGION.  
 OS Pseudomonas amyloclavata.  
 OC Bacteria; Proteobacteria.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SB-15;  
 RA Amezura A., Fujita M., Futai M.;  
 RL Submitted (NOV-1988) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: SIMILAR TO E. COLI ACETOHYDROXY ACID SYNTHASE.  
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 CC -----  
 DR EMBL: X13378; CAA31755.1; -  
 DR PIR: S01682; S01682.  
 DR HSSP: P37063; IPOM.  
 DR INTERPRO: IPR000399; -  
 DR PFAM: PF00205; TPP\_ENZYMES; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 396 AA; 42613 MW; EBAC54942050B03B CRC64;

Query Match	30.28;	Score 902.5;	DB 1;	Length 396;
Best Local Similarity	-49.08;	Pred. No. 3.6e-52;		
Matches 176; Conservative	72;	Mismatches 98;	Indels 13;	Gaps 4

[illegible]

RESULT	3	
ILVB_METJA		
ID	ILVB_METJA	STANDARD;
ACT25		PRT; 591 AA

DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE PROBABLE ACETOACETATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18) (AHAS)  
DE (ACETO)HYDROXY-ACID SYNTHASE LARGE SUBUNIT (AUS).

OS Methanococcus jannaschii.  
OC Archaea; Euryarchaeota; Methanococcales;  
OC Methanococcaceae  
RN Methanococcus.  
RN [1]

RP	SEQUENCE FROM N.A.
RC	STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

RA MEDLINE-9037555; PubMed-9008067;  
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Goc

RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Retch C.I.,  
RA Overbeek R., Kirkness E.F., Weltschlock K.G., Merilick J.M., Glodet A.,  
RA Scott J.L., Goodhagen S.M., Waldman T.P., Eubank T.D., Newman D.

RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.  
RA Cotton M.D., Roberts K.M., Hurst M.A., Kalne B.P., Borodovsky M.

RT "Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*,"  
 RT Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;  
 KX  
 KX

RL Science 273:1058-1073 (1996).  
CC -1- CATALYTIC ACTIVITY: 2-ACETOLACTATE + CO(2) = 2-PYRUVATE.  
-1- CATABOLISM: BUTYRATE CATABOLISM AND 2-ACETOLACTATE

CC -1- PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS  
CC SIMILARITY).  
CC CONCLUSION: INHIBITING FENOFIBRATE, AND MAGNESIUM ION (BI  
CC

CC -1- SUBUNIT: DIMER OF LARGE AND SMALL CHAINS (BY SIMILARITY).  
CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.  
CC -----

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CC -----  
DR EMBL: U67483; AAB98265.1; -.  
DR HSSBP; P06169; 1YPD.  
DR TIGR; MJ0277; -.  
DR INTERPRO: IPR000399; -.  
DR PFAM: PF00205; TPP\_enzymes; 1.  
DR PROSITE: PS00187; TPP\_ENZYMES; 1.  
KW Branched-chain amino acid biosynthes; Flavoprotein; Magnesium;  
KW Thiamine pyrophosphate; Lyase.  
FT ACY\_SITE 47 47 BY SIMILARITY.  
SQ SEQUENCE 591 AA; 64492 MW; DB39BC926D9B3A9D CRC64;

Query Match	19.68;	Score 586.5;	DB 1;	Length 591;
Best Local Similarity	29.58;	Pred. No. 3.2e-31;		
Matches 166;	Conservative 109;	Mismatches 247;	Indels 41;	Gaps 16;

QY 6 AEIIDIENAGVRRITGVGDSLNPIVDVROSDIEMVHVRNEEAAPFAAGSELTGE 65  
 Db 4 AEAIITKALEAGVATITGVPGAGALPRYDADLYDDHLITRIHQAAVHAAADGFAARSE 63  
 QY 66 LAVCAASGCPGNTLIGQLVDSHRNGAKVLAIAISHIPSAQISGTFPOETHPIIFKESG 125  
 Db 64 AGVCVSTGPGATNLVGIATAVADSSPVIALGQVPTKLIGNDAQGEIDALGLFMPITK 123  
 QY 126 YCEWNGEGGEQERLLHHAIGSTMAKGVSVVVIIPGDIANKEDAGDGT---SNSTISSGT 181  
 Db 124 HNFQIKRPEELIETFFRAAFETATTGRCGPVHIDLPKVDGDEIDIEKYPITPAVDVLPQYK 183

[illegible]

```

Db      244  FPEDHPLALGVWGHGHTKANVAVTECDVLIALGCRF--SDRVTGGDIRFAPEAKIINHID 301
Qy      292  INGAIHGRRTVVKPVYGDVAATIENTLP-----IYKEKTRDSFLDMILKAHERKSSVAV 346
Db      302  IDPEIKGNVRADPIVIGDKNKRVRLDIALALALEIDK--ETWLEIETVEL--KKSITPM 357

```

[illegible]

QY 401 DEVSFRHGTAMALPHAIGASVDBNRQVIAMCGGLGMLLGELTVKHLQLPLKAVV 460  
| : | ||| + |||| : || : |||| | || : : : || :

46] FNNSSIGMV-KIEMI.VEGOPFEETD-HEEVNEAFIAAAGCISVBTDDKKVBEOTAEAT 519

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Db      472  FDNRTLGMYQWONLYYGOQSEVHGLGSESPDFVKLAESYGVKADRIISPDIEKELKEAI 531

```

QY 519 AVPGVLDIVTDp-NAL-SIPP 539  
| | : | | | | | | : | |

Db 532 LSNEPYLLDIVIDPAEALLPMVPP 554

RESULT	4
POXB_LACPL	.

ID	POXR_LACPL	STANDARD;	PRT;	603 AA.
AC	P37063;			
DT	01-JUN-1994 (Rel. 29, Created)			

DT	01-OCT-1994 (Rel. 30, last sequence update)
DT	01-FEB-1995 (Rel. 31, last annotation update)
REFERENCE	1. 2. 3. 4. 5. 6. 7. 8. 9. 10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100. 101. 102. 103. 104. 105. 106. 107. 108. 109. 110. 111. 112. 113. 114. 115. 116. 117. 118. 119. 120. 121. 122. 123. 124. 125. 126. 127. 128. 129. 130. 131. 132. 133. 134. 135. 136. 137. 138. 139. 140. 141. 142. 143. 144. 145. 146. 147. 148. 149. 150. 151. 152. 153. 154. 155. 156. 157. 158. 159. 160. 161. 162. 163. 164. 165. 166. 167. 168. 169. 170. 171. 172. 173. 174. 175. 176. 177. 178. 179. 180. 181. 182. 183. 184. 185. 186. 187. 188. 189. 190. 191. 192. 193. 194. 195. 196. 197. 198. 199. 200. 201. 202. 203. 204. 205. 206. 207. 208. 209. 210. 211. 212. 213. 214. 215. 216. 217. 218. 219. 220. 221. 222. 223. 224. 225. 226. 227. 228. 229. 230. 231. 232. 233. 234. 235. 236. 237. 238. 239. 240. 241. 242. 243. 244. 245. 246. 247. 248. 249. 250. 251. 252. 253. 254. 255. 256. 257. 258. 259. 260. 261. 262. 263. 264. 265. 266. 267. 268. 269. 270. 271. 272. 273. 274. 275. 276. 277. 278. 279. 280. 281. 282. 283. 284. 285. 286. 287. 288. 289. 290. 291. 292. 293. 294. 295. 296. 297. 298. 299. 300. 301. 302. 303. 304. 305. 306. 307. 308. 309. 310. 311. 312. 313. 314. 315. 316. 317. 318. 319. 320. 321. 322. 323. 324. 325. 326. 327. 328. 329. 330. 331. 332. 333. 334. 335. 336. 337. 338. 339. 340. 341. 342. 343. 344. 345. 346. 347. 348. 349. 350. 351. 352. 353. 354. 355. 356. 357. 358. 359. 360. 361. 362. 363. 364. 365. 366. 367. 368. 369. 370. 371. 372. 373. 374. 375. 376. 377. 378. 379. 380. 381. 382. 383. 384. 385. 386. 387. 388. 389. 390. 391. 392. 393. 394. 395. 396. 397. 398. 399. 400. 401. 402. 403. 404. 405. 406. 407. 408. 409. 410. 411. 412. 413. 414. 415. 416. 417. 418. 419. 420. 421. 422. 423. 424. 425. 426. 427. 428. 429. 430. 431. 432. 433. 434. 435. 436. 437. 438. 439. 440. 441. 442. 443. 444. 445. 446. 447. 448. 449. 450. 451. 452. 453. 454. 455. 456. 457. 458. 459. 460. 461. 462. 463. 464. 465. 466. 467. 468. 469. 470. 471. 472. 473. 474. 475. 476. 477. 478. 479. 480. 481. 482. 483. 484. 485. 486. 487. 488. 489. 490. 491. 492. 493. 494. 495. 496. 497. 498. 499. 500. 501. 502. 503. 504. 505. 506. 507. 508. 509. 510. 511. 512. 513. 514. 515. 516. 517. 518. 519. 520. 521. 522. 523. 524. 525. 526. 527. 528. 529. 530. 531. 532. 533. 534. 535. 536. 537. 538. 539. 540. 541. 542. 543. 544. 545. 546. 547. 548. 549. 550. 551. 552. 553. 554. 555. 556. 557. 558. 559. 560. 561. 562. 563. 564. 565. 566. 567. 568. 569. 570. 571. 572. 573. 574. 575. 576. 577. 578. 579. 580. 581. 582. 583. 584. 585. 586. 587. 588. 589. 590. 591. 592. 593. 594. 595. 596. 597. 598. 599. 600. 601. 602. 603. 604. 605. 606. 607. 608. 609. 610. 611. 612. 613. 614. 615. 616. 617. 618. 619. 620. 621. 622. 623. 624. 625. 626. 627. 628. 629. 630. 631. 632. 633. 634. 635. 636. 637. 638. 639. 640. 641. 642. 643. 644. 645. 646. 647. 648. 649. 650. 651. 652. 653. 654. 655. 656. 657. 658. 659. 660. 661. 662. 663. 664. 665. 666. 667. 668. 669. 670. 671. 672. 673. 674. 675. 676. 677. 678. 679. 680. 681. 682. 683. 684. 685. 686. 687. 688. 689. 690. 691. 692. 693. 694. 695. 696. 697. 698. 699. 700. 701. 702. 703. 704. 705. 706. 707. 708. 709. 710. 711. 712. 713. 714. 715. 716. 717. 718. 719. 720. 721. 722. 723. 724. 725. 726. 727. 728. 729. 730. 731. 732. 733. 734. 735. 736. 737. 738. 739. 740. 741. 742. 743. 744. 745. 746. 747. 748. 749. 750. 751. 752. 753. 754. 755. 756. 757. 758. 759. 760. 761. 762. 763. 764. 765. 766. 767. 768. 769. 770. 771. 772. 773. 774. 775. 776. 777. 778. 779. 780. 781. 782. 783. 784. 785. 786. 787. 788. 789. 790. 791. 792. 793. 794. 795. 796. 797. 798. 799. 800. 801. 802. 803. 804. 805. 806. 807. 808. 809. 810. 811. 812. 813. 814. 815. 816. 817. 818. 819. 820. 821. 822

05 *Flavobacterium salinarum* (CC 12.2.1.1) (FV04).  
06 *Lactobacillus plantarum*.  
07 Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;  
08

OC Lactobacillus.  
RN [1]  
RP X-RAY CRYSTALLOGRAPHY (2.5 AND 2.1 ANGSTROMS) OF WILD-TYPE AND MUTANT

RX MEDLINE=94194507; PubMed=8145244;  
RA Muller Y.A., Schumacher G., Rudolph R., Schulz G.E.;

RT	"The refined structures of a stabilized mutant and of wild-type
RT	pyruvate oxidase from <i>Lactobacillus plantarum</i> .";
RL	J. Mol. Biol. 237:315-335(1994).
RN	[2]
RP	X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX	MEDLINE=93174262; PubMed=8438155;
RA	Muller Y.A., Schulz G.E.;
RT	"Structure of the thiamine- and flavin-dependent enzyme pyruvate
RT	oxidase.";
RL	Science 259:965-967(1993).
CC	-1- FUNCTION: IMPORTANT FOR THE AEROBIC GROWTH. DECARBOXYLATES
CC	PYRUVATE IN FOUR STEPS. THE ENERGY RELEASED IS PARTIALLY STORED
CC	IN ACETYL PHOSPHATE.
CC	-1- CATALYTIC ACTIVITY: PYRUVATE + ORTHOPHOSPHATE + O(2) + H(2)O =
CC	ACETYL PHOSPHATE + CO(2) + H(2)O(2).
CC	-1- COFACTOR: THIAMINE PYROPHOSPHATE, FAD AND MAGNESIUM ION.
CC	-1- SUBUNIT: HOMOTETRAMER.
CC	-1- DOMAIN: EACH MONOMER IS DIVIDED INTO THREE DOMAINS, EACH OF WHICH
CC	CONTAINS A SIX-STRANDED PARALLEL BETA SHEET SURROUNDED BY ALPHA
CC	HELICES.
CC	-1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
DR	PDB: IPOW; 31-JAN-94.
DR	PDB: IPOX; 31-JAN-94.
DR	INTERPRO: IPR000399; -
DR	PFAM: PF00205; TPP_enzymes; 1.
DR	PROSITE: PS00187; TPP_ENZYMES; 1.
KM	Oxidoreductase; Flavo-protein; FAD; Thiamine pyrophosphate; Magnesium;
KM	3D-structure.
FT	DOMAIN 1 191 CORE.
FT	DOMAIN 192 342 FAD.
FT	DNAIN 343 603 TPP.
FT	ACT_SITE 59 59 BY SIMILARITY.
FT	METAL 447 447 MAGNESIUM.
FT	METAL 474 474 MAGNESIUM.
FT	METAL 476 476 MAGNESIUM.
FT	STRAND 10 12
FT	HELI 13 23
FT	TURN 24 25
FT	STRAND 28 31
FT	HELI 35 46
FT	TURN 47 50
FT	STRAND 52 55
FT	HELI 59 73
FT	STRAND 77 81
FT	TURN 83 84
FT	HELI 85 88
FT	TURN 89 90
FT	HELI 91 99
FT	TURN 100 101
FT	STRAND 104 110
FT	TURN 113 117
FT	HELI 121 122
FT	TURN 127 130
FT	STRAND 131 133
FT	HELI 136 139
FT	TURN 144 145
FT	HELI 146 160
FT	TURN 161 161
FT	STRAND 163 169
FT	TURN 170 171
FT	HELI 172 174
FT	STRAND 176 178
FT	TURN 179 180
FT	HELI 186 188
FT	STRAND 196 196
FT	HELI 199 211
FT	STRAND 215 219
FT	HELI 221 237
FT	TURN 238 238
FT	STRAND 241 243
FT	HELI 245 247
FT	TURN 248 249
FT	HELI 253 254
FT	TURN 253 254

Query Match	Best Local Similarity	Score	DB 1;	Length	DB 2;
Matches 147; Conservative 116; Mismatches 251; Indels 20; Gaps 8	18.8%;	560;	DB 1;	603;	
	27.5%;	Pred. No. 1.8e-29;			
9 LIDTLEAGCVKRIYGLVGSNLPYDAV--KOSDIEWHVHRNDEAAAFAGAESLITGL 66	17 VIKLEAWCVLDHVLPGGSGINSIMDALSAERDRHYIOVRHEEVGAMAAADAKLTGKI 76	67 AACAACGCGGNHLLGGTDSHRNGAKVLAISHIPSAQIGSPFQETPELIFKESGY 126	77 GVCFGSAGGGHLMGLGDARDHVPVLTALIGFETGMNMDTFOEMNENPIYADVDY 136	127 CEMVNGEGEGERILHAIHISTWAGKGVSVVPIGDIKEDAGDGYNSNSTISSGPPV-F 185	137 NNTVNAALPHVIDAIRKRAYAHGQVAVQIIPVDLPQOIAEDWYASANSYQPLDE 196
186 PDPTAALVEAIINNAKSVTLFCGAGCVKNAQVLELAEKIKSPIGHALGKQYIOHNP 245	197 PVOQAVTRILQTLAERPLIYVIGARRAKKELEQISTKLKIPLMSTYPAKGIADRPV 256	246 FEVGMGSLIGYACVDASNEADLLILGTDFPSD---FLPRDNVAQVDINGAHIGRT 301	257 AYLGSANRYAQRPAEMALAAQADVLFVGNNYPAEVSKAFTKTRVFLQIDIDPAKLGKH 316	302 IVKYPATGGVAATIEHILPHVKEKTRSLDRML--KAHERKLSSVVEYTHNNEKHP 358	317 KRIDIAVLADQKTLAAILQVSEKRETPMWOQANLAVKMKRAYLASED-----KQEGP 370



OC Eukaryota: Cryptophyta; Cryptomonadaceae; Guillardia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99128221; PubMed=9929392;  
 RA Douglas S.E., Penny S.L.;  
 RT "The plastid genome of the cryptophyte alga, Guillardia theta:  
 complete sequence and conserved syntenic groups confirm its common  
 ancestry with red algae.";  
 RL J. Mol. Evol. 48:236-244(1999).  
 CC -1- CATALYTIC ACTIVITY: 2-ACETOYLACTATE + CO(2) = 2-PYRUVATE.  
 CC -1- COFACTOR: THIAMINE PYROPHOSPHATE, AND MAGNESIUM ION  
 CC (BY SIMILARITY).  
 CC -1- PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.  
 CC -1- SUBUNIT: DIMER OF LARGE AND SMALL CHAINS (BY SIMILARITY).  
 CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.  
 CC -----  
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 CC -----  
 CC EMBL: AF041468; AAC35740.1; -  
 CC INTERPRO: IPR000399; -  
 DR PFAM: PF00205; TPP-ENZYMES; 1.  
 DR PROSITE: PS00187; TPP-ENZYMES; 1.  
 KW branched-chain amino acid biosynthesis; Flavoprotein; Magnesium;  
 KM Thiamine pyrophosphate; Lyase; Chloroplast.  
 FT ACT SITE 60 BY SIMILARITY.  
 SQ SEQUENCE 575 AA: 63359 MW: F9447F9A178D3EC4 CRC64;

Query Match 17.9%; Score 533.5; DB 1; Length 575;  
 Best Local Similarity 28.0%; Pred. No. 9,1e-28;  
 Matches 161; Conservative 114; Mismatches 251; Indels 49; Gaps 17;

QY 9 LIDTLEAGQVKRYGLVGSUNPIYDAV-----RQSDIEVHVRNEEAFAAGASGLING 64  
 DB 16 LIDSLVRHGVKFIHFGYGGALIPYDELAYAMEKEGFTIEHLVRHGGASHASGJARSTG 75  
 QY 65 ELAVCAASGPGNTLHIOGLYDSHRNGAKVLAISHIPSAQIGSTFQF-----THPEI 118  
 DB 76 NVCVCATSGPKNLTNLTGATAMDSVMVITIGOVSGSLGTDAFQEVDFEGTLPY 135  
 QY 119 ---LFKESGCEVMVNGGEGERTIIHNAIOSTMACKGVSVVYIPDDIKEDAGDGTYSN 174  
 DB 136 KHSYVVRERK-----EMGRIVAESFFIAKYGRRPVLLIDPKDVGLEKFDYQVNP 186  
 QY 175 STTS-SGTPVVP-DPTFAALVEALINNAKSVTLFCGAG--VKNARAQVLELAERIKSPI 230  
 DB 187 NNINLACGVKLVKNDONRISOANLTKQSSQPLLYTGGCAVNSINNELINLAKIYV 246  
 QY 231 GHALGKROYLOHNPPEVNGSLIGYACVDASNEADLLILGLTF-----PYSDFLEK 284  
 DB 247 ATTLMGKGIIDESHPLSLGMLGCHGTUANYAVSECDLLIALCARPDRVTGKIDEFACH 306  
 QY 285 DNAOAVDINGAHNGRTYKYPRTGVAAATIEHLPHVAKETRSPLDRLNKAHEKISS 344  
 DB 307 AOVIHVIDPAETIGKNTPOIGIVGEIKDFVRLIECL--KNDINFDSEOSQAWRSRIIR 364  
 QY 345 VVEVYTHNVKHY-PIHPEVASILNELADR--DAVETVDTGCMVHARYLNPPEGTBD 401  
 DB 365 WKREYPLVLPKNNINLSPQ---EVIHEISTEATNAYFTTVDGQHQMAAQFITSQ--KR 419  
 QY 402 EVGSEFRHGTMANALPHAQAQSVDRNRQYIAMCGDGLGLMLGELLTKLHQLPLKAAVYF 461  
 DB 420 WITSAGIGTWGGLPAIPAIGQIAHPNEQVYICISGDASFQNNIOELGTVSQYGPRIKIFII 479  
 QY 462 NNSLSLGMVK-LEMLVGCQPEFTGDHEE--VNFALIAAAGIKSVRTIDPKKVEQOLAEL 518  
 DB 480 NNMWQWVROMQOAFYGERYSNMEKGAENFTKVAEALFSLKTKSRNDLKRILEAL 539

QY 519 AYPGVILIDI--VTDPNAL-SIPPTTQWYGFSS 550  
 DB 540 DYDGEILVDIYADENCYPMVAPCKSNAGMGIN 574

RESULT 7  
 ID ILVB\_PORPU STANDARD; PRT; 590 AA.  
 AC P31594;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE ACETOYLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18) (AHAS)  
 DE (ACETOHYDROXY-ACID SYNTHASE LARGE SUBUNIT) (ALS).  
 GN ILVB.  
 OS Porphyra purpurea, and Porphyra umbilicalis (Laver).  
 OG Chloroplast.  
 OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=P.PURPUREA; STRAIN=AVONPORT;  
 RA Reith M.E., Munnolland J.;  
 RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast  
 genome.";  
 RN Plant Mol. Biol. Rep. 13:333-335(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=P.UMBILICALIS; STRAIN=AVONPORT;  
 RX MEDLINE=93153832; PubMed=8381336;  
 RA Reith M., Munnolland J.M.;  
 RT "Two amino-acid biosynthetic genes are encoded on the plastid genome  
 of the red alga Porphyra umbilicalis.";  
 RT Curr. Genet. 23:59-65(1993).  
 CC -1- CATALYTIC ACTIVITY: 2-ACETOYLACTATE + CO(2) = 2-PYRUVATE.  
 CC -1- COFACTOR: THIAMINE PYROPHOSPHATE, AND MAGNESIUM ION  
 CC (BY SIMILARITY).  
 CC -1- PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.  
 CC -1- SUBUNIT: DIMER OF LARGE AND SMALL CHAINS (BY SIMILARITY).  
 CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.  
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 CC -----  
 CC EMBL: U38804; AAC08216.1; -  
 DR EMBL: M94625; AAA03052.1; -  
 DR PIR: S27402; S27402.  
 DR PIR: S28920; S28920.  
 DR HSP: P06169; 1YPD.  
 DR INTERPRO: IPR000399; -  
 DR PFAM: PF00205; TPP-ENZYMES; 1.  
 DR PROSITE: PS00187; TPP-ENZYMES; 1.  
 KW branched-chain amino acid biosynthesis; Flavoprotein; Magnesium;  
 KM Thiamine pyrophosphate; Lyase; Chloroplast.  
 FT ACT SITE 61 BY SIMILARITY.  
 SQ SEQUENCE 590 AA: 64929 MW: 1C35F7DF0F2E57AD CRC64;

Query Match 17.9%; Score 533.5; DB 1; Length 590;  
 Best Local Similarity 27.8%; Pred. No. 9,4e-28;  
 Matches 161; Conservative 107; Mismatches 256; Indels 55; Gaps 14;

QY 9 LIDTLEAGQVKRYGLVGSUNPIYDAV-----RQSDIEVHVRNEEAFAAGASGLING 64  
 DB 17 LIDSLVRHGVKFIHFGYGGALIPYDELAYAMEELSLIKNMLVRHGGASHADAVSRSTG 76  
 QY 65 ELAVCAASGPGNTLHIOGLYDSHRNGAKVLAISHIPSAQIGSTFQFQTHPEILFKES 124





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RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85242084; PubMed=2989782;
RA Mek R.C., Hauser G.A., Hatfield G.W.;
RT "The nucleotide sequence of the ilvB operon of Escherichia coli:
RT sequence homologues of the acetylhydroxy acid synthase isozymes.";
RL Nucleic Acids Res. 13:3995-4010(1985).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=85242083; PubMed=2989781;
RA Friden P., Donegan J., Mullen J., Tsui P., Freundlich M.;
RT "The ilvB locus of Escherichia coli K-12 is an operon encoding both
RT subunits of acetylhydroxyacid synthase I.";
RL Nucleic Acids Res. 13:3979-3993(1985).
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=K12 / MG1655;
RA MEDLINE=93315143; PubMed=7686882;
RA Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
RT "DNA sequence and analysis of 136 kilobases of the Escherichia coli
RT genome: organizational symmetry around the origin of replication.";
RL Genomics 16:551-561(1993).
CC -1- CATALYTIC ACTIVITY: 2-ACETOLACTATE + CO(2) = 2-PYRUVATE (THIS
CC ENZYME ALSO CATALYZES FORMATION OF 2-ACETO-2-HYDROXYBUTANOATE).
CC -1- COFACTOR: THIAMINE PYROPHOSPHATE, AND MAGNESIUM ION.
CC -1- PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.
CC -1- SUBUNIT: DIMER OF LARGE AND SMALL CHAINS.
CC -1- MISCELLANEOUS: E.COLI CONTAINS GENES FOR 3 AHAS ISOZYMES: ILVBN,
CC ILVGM AND ILVH.
CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
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CC -----
DR EMBL: J01633; AAA24017.1; -
DR EMBL: X02541; CAA26387.1; -
DR EMBL: L10328; AAA62023.1; -
DR EMBL: AE000444; AAC76694.1; -
DR PIR: A23803; YCECIL.
DR SWISS-2DPAGE: P08142; COLI.
DR ECODBASE: D057.0; 6TH EDITION.
DR ECOGENE: B610494; ILVB.
DR INTERPRO: IPR000399; -
DR PFAM: PF00205; TPP_enzymes; 1.
DR PROSITE: PS00187; TPP_ENZYMES; 1.
KW Branched-chain amino acid biosynthesis; Flavoprotein; Magnesium;
KW Thiamine pyrophosphate; Lyase.
FT ACT_SITE 60
FT SEQUENCE 562 AA; 60440 MW; 70F8A3128031553C CRC64;
SQ

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Query Match 17.5%; Score 523.5; DB 1; Length 562;
Best Local Similarity 27.9%; Pred. No. 4e-27;
Matches 162; Conservative 108; Mismatches 239; Indels 71; Gaps 17;

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DB 196 FSEESI-----RDAAAM---INAAKRPVLVYLGSGVINAPAVRBLAEKAOLEPTT 241
QY 232 HALCGKOYIOENPEFEVMSGILGYGACVASNADLLILGLTDFE-----PVSDFPKD 285
DB 242 MTLMALMGKRAHPLSLGMLGMGVSRSTNYILOADLLIYAGFDRDRAIGKEQFCFPA 301
QY 286 NVAQVDINGAHIGRTTVKYP---VTGDVAATENIILPHYKEKTRSFELDRMLKAHERK 341
DB 302 KIIVHVDIDRAELGR---IKOPHVALQADVDDVLAQLIPLV-EAQPRAEWHQIVADQREF 357
QY 342 ---LSVVEYTYTHNVEKHPVPIHPEYVASINELA---DKDAVFTVDTGMCNWHAR--1 393
DB 358 PCPIPKACDPLSH-----YGLINVAACVDNNAITTTVDGQHQMWTACAYPL 404
QY 394 ENPEGTRDFVSGFRHGTMANALPHALGAQSVDRROYIANMGDGLMLIGELTLVKHQ 453
DB 405 NRP---RQMLTSGGLGTMGFLPAIGALANPDKRYLCSSGDSLMNTOENATASENQ 461
QY 454 LPLKAVFNNSLSGMV-KLEMLVEGOPEFTDHE-EVNFAEIATAAGIKSVRTDPKRV 511
DB 462 LDVITILMNNAALGIVHQOQSLFYEGCGFAATYFGKINFMQIAGFGLETCDLNNEADPQ 521
QY 512 EQLAEALVPGPVLIDVTPNAL----SIPTWEQVYG 548
DB 522 ASLQEIINRPGPALIHVRIDAEKRYVPMVPPGAANTEWVG 561

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RESULT 10
ILVB_SPIPL STANDARD: PRT: 579 AA.
ID ILVB_SPIPL
AC P27868;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ACETOLACTATE SYNTHASE (EC 4.1.3.18) (ACETOHYDROXY-ACID SYNTHASE) (ALS)
DE (FRAGMENT).
GN IlvY.
OS Spirulina platensis.
OC Bacteria; Cyanobacteria; Oscillatoriales; Spirulina.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=923814877; PubMed=1512571;
RA Milano A., de Rossi E., Zanaria E., Barbierato L., Ciferri O.,
RA Riccardi G.;
RT "Molecular characterization of the genes encoding acetylhydroxy acid
RT synthase in the cyanobacterium Spirulina platensis.";
RL J. Gen. Microbiol. 138:1399-1408(1992).
CC -1- CATALYTIC ACTIVITY: 2-ACETOLACTATE + CO(2) = 2 PYRUVATE.
CC -1- COFACTOR: THIAMINE PYROPHOSPHATE, AND MAGNESIUM ION.
CC -1- PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.
CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
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DR EMBL: M75907; AAA26595.1; -
DR PIR: B44857; B44857.
DR HSSP: P06169; IYPD.
DR INTERPRO: IPR000399; -
DR PFAM: PF00205; TPP_enzymes; 1.
DR PROSITE: PS00187; TPP_ENZYMES; PARTIAL.
KW Branched-chain amino acid biosynthesis; Flavoprotein; Lyase;
KW Thiamine pyrophosphate.
FT ACT_SITE 61
FT NON_TER 579
FT SEQUENCE 579 AA; 63440 MW; BC94FEA728A7889A CRC64;

```







01-OCT-2000 (rel. 40, last annotation update)  
ACETOLACTATE SYNTHASE PRECURSOR (EC 4.1.3.18) (ACETOHYDROXY-ACID  
SYNTHASE) (ALS).  
GN CSR 1.2.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta:  
OC Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eurosids II:  
OC Brassicales: Brassicaceae: Arabidopsis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CV. COLUMBIA:  
RX MEDLINE-90245681: Pubmed-2336405:  
RA Sathasivan K., Haughn G.W., Mural N.;  
RT "Nucleotide sequence of a mutant acetolactate synthase gene from an  
imidazolone-resistant Arabidopsis thaliana var. Columbia.";  
RL Nucleic Acids Res. 18:2188-2188(1990).  
RN [2]  
RP VARIANT GH90.  
RC STRAIN-CV. COLUMBIA:  
RA Sathasivan K., Haughn G.W., Mural N.;  
RT "Molecular basis of imidazolone herbicide resistance in Arabidopsis  
thaliana var Columbia.";  
RL Plant Physiol. 97:1044-1050(1991).  
CC -1- CATALYTIC ACTIVITY: 2-ACETO-LACTATE + CO(2) = 2-PYRUVATE (THIS  
CC ENZYME ALSO CATALYZES FORMATION OF 2-ACETO-2-HYDROXY-BUTANOATE).  
CC -1- COFACTOR: THIAMINE PYROPHOSPHATE, AND MAGNESIUM ION.  
CC -1- PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.  
CC -1- MISCELLANEOUS: ACETO-LACTATE SYNTHASE IS THE TARGET ENZYME FOR  
CC SULFONYLUREA AND IMIDAZOLINONE HERBICIDES. MUTANT GH 90 IS  
CC RESISTANT TO IMIDAZOLINONE HERBICIDES AND MUTANT GH 50 TO  
CC SULFONYLUREA.  
CC -1- BIOTECHNOLOGY: INTRODUCED BY GENETIC MANIPULATION AND EXPRESSED IN  
CC SULFONYLUREA RESISTANT FLAX BY THE UNIVERSITY OF SASKATCHEWAN.  
CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.  
CC -----  
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CC -----  
CC EMBL: X51514; CAA35887.1; -  
CC DR PIR: S09502; YCMU.  
CC DR HSSP: P06169; 1YPD.  
CC DR INTERPRO: IPR000399; -  
CC DR PFAM: PF00205; TPP\_ENZYMES; 1.  
CC DR PROSITE: PS00187; TPP\_ENZYMES; 1.  
CC KW Branched-chain amino acid biosynthesis; Flavoprotein; Magnesium;  
KW Thiamine pyrophosphate; Herbicide resistance; Transist peptide;  
KW Lyase; Chloroplast; Genetically modified food.  
FT TRANSIT 1 97  
FT CHAIN 98 670  
FT ACT\_SITE 144 144 ACETO-LACTATE SYNTHASE.  
FT FT 197 197 BY SIMILARITY.  
FT VARIANT 653 653 P -> S (IN MUTANT GH 50).  
FT VARIANT 653 653 S -> N (IN MUTANT GH 90).  
FT SEQUENCE 670 AA: 72585 MW: 84697860.155160 CRC64;  
Query Match 16.5% Score 493; DB 1: Length 670;  
Best Local Similarity 27.5% Pred. No. 5e-25;  
Matches 158; Conservative 97; Mismatches 259; Indels 60; Gaps 14;

220 KHNVLWMDVEDIPRIIEEAFPLATSGRPGPVLDVDEKDI-QOOLAIPNMEQARLPGYMS 278  
184 VFPDPTEAAL---VEAINNAKSVTLFCGAGVKNARAQVLEAKIKSPIGHALGKQYI 240  
279 RMPKPPEDSHLEQIVRLISESKRPVLYVGGCLNSSDELSREVELTGIPASTYMLGSGY 338  
241 QHENPFEVGMGSLGACVDASNEADLLILGTD-PSDFLPKPDNVAQYDING 294  
339 PCDDLSLHMLGMHGTIVYANVAVESHDLARFVRDDVYTGLEAFASAKIVHIDIDS 398  
295 AHIGRTTYKYPVTDVAATENILPHVKEKIDRSFLDRNL-KAHERKLSVETTYTIN 352  
399 AEGIKKKTPTVHSCGVKALDQ-----MNKVLERABELKIDFGVMRNEIN 445  
353 VEKH-----VPIHEVYASLINELADKAVTYVDTGKMNVMHARTIEMPECTRDP 402  
446 VOKOKFPISFKTFGEAIPPOYAIKVLDELTDGKAILSTGVGHOMAAOFP-NYKKPRQW 504  
403 VGSFRHGTMANALPHIAGASVDNRQVIAKMGDGLMGLGELLTVKLHQLPLKAVFN 462  
505 LSSGGLGAMGFLGPAIGASVANPDAIVDDIDGGSFIMNVDELATIRVENLPVKLLN 564  
463 NSSLGWVKLEMEVE-----GOPEFGTDHEV--NFAEITMAAGIKSVRTDP 507  
565 NQHLGVV---MQMEDRFYKANRAHFTLGP---AQDEIFPNMLLPMAACGIPAAVATYK 618  
508 KKYREQLAEALAPGVLDIVDPNALSTPPI 541  
619 ADLEAIGTMLDTPGPLYLDVIC-PRQEHVPLMI 651  
RESULT 14  
ID POXB\_STRPN STANDARD; PRT: 591 AA.  
AC 054970;  
DT 15-DEC-1998 (rel. 37, Created)  
DT 15-DEC-1998 (rel. 37, Last sequence update)  
DT 15-DEC-1998 (rel. 37, Last annotation update)  
DE PYRUVATE OXIDASE (EC 1.2.3.3) (PYRUVIC OXIDASE) (POX).  
GN SPXB.  
OS Streptococcus pneumoniae.  
OC Bacteria: Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
OC Streptococcus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-R6X.  
RX MEDLINE-96417859: Pubmed-8820650;  
RA Spellerberg B., Cundell D.R., Sanders J., Pearce B.J.,  
RA Idanpaan-Heikkila I., Rosenow C., Masure H.R.;  
RT "pyruvate oxidase, as a determinant of virulence in Streptococcus  
pneumoniae.";  
RL Mol. Microbiol. 19:803-813(1996).  
CC -1- FUNCTION: IMPORTANT FOR THE AEROBIC GROWTH. DECARBOXYLATES  
CC PYRUVATE IN FOUR STEPS. THE ENERGY RELEASED IS PARTIALLY STORED  
CC IN ACETYL PHOSPHATE (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: PYRUVATE + OPHOSPHATE + O(2) + H(2)O -  
CC ACETYL PHOSPHATE + CO(2) + H(2)O(2).  
CC -1- COFACTOR: THIAMINE PYROPHOSPHATE, FAD AND MAGNESIUM ION (BY  
CC SIMILARITY).  
CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.  
CC -----  
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CC -----  
CC EMBL: U39074; AAB40976.1; -  
CC DR INTERPRO: IPR000399; -  
CC DR PFAM: PF00205; TPP\_ENZYMES; 1.

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RL Mol. Gen. Genet. 229:31-40(1991)
CC -i- CATALYTIC ACTIVITY: 2-ACETOGLUTATE + CO(2) = 2-PYRUVATE (THIS
CC ENZYME ALSO CATALYZES FORMATION OF 2-ACETO-2-HYDROXY-BUTANONATE).
CC -i- COFACTOR: THIAMINE PYROPHOSPHATE, AND MAGNESIUM ION.
CC -i- PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.
CC -i- MISCELLANEOUS: ACETOGLUTATE SYNTHASE IS THE TARGET ENZYME FOR
CC SULFONYLUREA AND IMIDAZOLINONE HERBICIDES.
CC -i- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
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CC -----
DR EMBL; Z11524; CAA7613.1; -.
DR PIR; S17691; S17691.
DR HSSP; P06169; 1YPD.
DR INTERPRO; IPR000399; -.
DR PFAM; PF00205; TPP_enzymes; 1.
DR PROSITE; PS00187; TPP_ENZYMES; 1.
DR BRANCHED-CHAIN amino acid biosynthesis; Flavoprotein; Magnesium;
KW Thiamine pyrophosphate; Herbicide resistance; Transit peptide;
KW lyase; Chloroplast; Multigene family.
FT TRANSIT 1 82 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 83 655 ACETOGLUTATE SYNTHASE I.
FT ACT_SITE 129 129 BY SIMILARITY.
SQ SEQUENCE 655 AA; 71288 MW; 1B6AD7D7A0DAD91A CRC64;

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DB 612 TMLDTPGVLDDVIC-PHOENVLPMI 636

Search completed: March 17, 2001, 21:58:58  
Job time: 394 sec

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